

SEQUENCE LISTING

<110> Heinrichs, Jon
Johnson, Leslie S.
Koenig, Scott
Adamou, John E.

<120> Pneumococcal Protein Homologs and Fragments for
Vaccines

<130> 469201-402

<140>
<141>

<150> U.S. 60/150,750
<151> 1999-08-25

<160> 6

<170> PatentIn Ver. 2.1

<210> 1
<211> 2478
<212> DNA
<213> Streptococcus pyogenes

<400> 1
gtgaagaaaa catatggta tatcggtca gttgctgcta ttttacttagc tactcatatt 60
ggaagttacc aaccttgtaa gcatcatatg gtttcagcaa caaaggacaa tcaaattgcc 120
tatattgtat atagcaaagg taaggaaaa gcccctaaaa caaacaaaac gatggatcaa 180
atcagtgcgt aagaaggcat ctctgctgaa cagatcgtag tcaaaattac tgaccaaggc 240
tatgtgaccc cacatggta ccattatcat ttttacaatg ggaaagtcc ttatgtgcg 300
attattatgt aagagtgtt gatgacggat cctaattacc gttttaaaca atcagacgtt 360
atcaatgaaa tcttagacgg ttacgttatt aaagtcaatg gcaactatta tgtttaccc 420
aaggccaggta gcaagcgc当地 aaacattcga accaaacaac aaattgctga gcaagtagcc 480
aaaggaacta aagaagctaa agaaaaagggt ttagtcaag tggcccatct cagtaaagaa 540
gaaggcgg cagtcataatg agcaaaaaaga caaggacgt atactacaga cgatggctat 600
atttttatgc ctagcagatatt cattgtatgt ttaggatgt ctatattatgt acctcatgg 660
aatcaatcatttattcc taaaaaggat ttgtctccaa gtgagctgc tgctgcacaa 720
gcctacttggaa gtcaaaaaca aggtcgaggt gctagaccgt ctgattaccg cccgacacca 780
gccccagccc caggtcgtag gaaagccccaa attcctgtatg tgacgcctaa ccctggacaa 840
ggtcatcagc cagataacgg tggctatcat ccagcgcctc ctaggccaat tgatgcgtca 900
caaaacaaac accaaagaga tgagttaaa ggaaaaacact ttaaggaact tttagatcaa 960
ctacaccgtc ttgatgttggaa ataccgtcat gtggaagaag atgggttgc ttgtgaaccc 1020
actcaagtga tcaaataaaa cgctttggg tatgtgggtgc ctcatggaga tcattatcat 1080
attatccaa gaagtcagtt atcacctt gaaatggaaat tagcagatcg atacttagcc 1140
ggccaaactg aggacgtatc ctcaggttca gatcaactcaa aaccatcaga taaagaagtg 1200

D
E
P
E
C
T
I
O
N
S
P
R
E
D
I
C
T
I
O
N
S

acacataccct ttcttggta tcgcataaaa gcttacggaa aaggcttaga tggtaaacca 1260
tatgatacga gtatgtctt tgtttttagt aaagaatcca ttcattcagt ggataaaatca 1320
ggagttacag ctaaacacgg agatcatttc cactatatag gattggaga acttgaacaa 1380
tatgagttgg atgaggtcgc taactgggtg aaagcaaaaag gtcagaactg tgagcttgct 1440
gctgcttgg atcaggaaca aggcaaagaa aaaccactct ttgacactaa aaaagtgagt 1500
cgcaaaatgaa caaaagatgg taaaatggc tatatgtgc caaaagatgg caaggactat 1560
ttctatgctc gtatgtact tgatttgact cagattgcct ttgccgaaca agaactaatg 1620
ctttaagata agaaacatta cggttatgac atttgtgaca caggtattga gccacgactt 1680
gctgttagatg tgtcaagtct gccgatgcat gctggtaatg ctacttacga tactggaaatg 1740
tcggttggta tccctcatat tgatcatatc catgtcggtc cgtattcatg gttgacgcgc 1800
gatcagattg caacaatcaa gatgtgtatg caacaccccg aagttcgcc ggatatatgg 1860
tctaaggccag ggcataaga gtcagggtcg gtcattccaa atgttacgccc tcttgataaa 1920
cgtgctgta tgccaaactg gcaaaattatc catttgcgtg aagaagttca aaaaggcccta 1980
gcagaagggtc gttttgcac accagacggc tatatttcg atccacgaga tggttggcc 2040
aaagaaaactt ttgtatggaa agatggctcc tttagcatcc caagacgaga tggcagttca 2100
ttgagaacca ttaataaaatc tgatctatcc caagctgatg ggcaacaagc tcaagagtt 2160
ttggccaaaga aaaacgctgg tgatgtact gatacggata aacccaaaga aaagcaacag 2220
gcagataaga gcaatgaaaa ccaacagccca agtgaagccca gtaaagaaga agaaaaagaa 2280
tcagatgact ttatagacag ttaccagac tatggcttag atagagcaac cctagaagat 2340
catatcaatc aattagcaca aaaagctaat atcgatccta agtatctcat tttccaacca 2400
gaaggtgtcc aattttataa taaaaatggt gaatttggtaa cttatgatcaagacactt 2460
caacaatcaa acccttaa 2478

<210> 2

<211> 825

<212> PRT

<213> Streptococcus pyogenes

<400> 2
Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
1 5 10 15
Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Ser

20 25 30
Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
35 40 45
Ala Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu

50 55 60
Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
65 70 75 80
Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val

85 88 90 95
2

Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
 100 105 110
 Tyr Arg Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
 115 120 125
 Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
 130 135 140
 Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
 145 150 155 160
 Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
 165 170 175
 Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
 180 185 190
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
 195 200 205
 Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
 210 215 220
 Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
 225 230 235 240
 Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
 245 250 255
 Arg Pro Thr Pro Ala Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro
 260 265 270
 Asp Val Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly
 275 280 285
 Tyr His Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His
 290 295 300
 Gln Arg Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln
 305 310 315 320
 Leu His Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu
 325 330 335
 Ile Phe Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val
 340 345 350

Val Pro His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser
355 360 365
Pro Leu Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Glu
370 375 380
Asp Asp Asp Ser Gly Ser Asp His Ser Lys Pro Ser Asp Lys Glu Val
385 390 395 400
Thr His Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu
405 410 415
Asp Gly Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu
420 425 430
Ser Ile His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp
435 440 445
His Phe His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp
450 455 460
Glu Val Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Ala
465 470 475 480
Ala Ala Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr
485 490 495
Lys Lys Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Met
500 505 510
Met Pro Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Asp Gln Leu Asp
515 520 525
Leu Thr Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys
530 535 540
Lys His Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu
545 550 555 560
Ala Val Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr
565 570 575
Asp Thr Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val
580 585 590
Val Pro Tyr Ser Trp Leu Thr Arg Asp Gln Ile Ala Thr Ile Lys Tyr
595 600 605

Val Met Gln His Pro Glu Val Arg Pro Asp Ile Trp Ser Lys Pro Gly
 610 615 620
 His Glu Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys
 625 630 635 640
 Arg Ala Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Glu Val
 645 650 655
 Gln Lys Ala Leu Ala Glu Gly Arg Phe Ala Thr Pro Asp Gly Tyr Ile
 660 665 670
 Phe Asp Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp
 675 680 685
 Gly Ser Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile
 690 695 700
 Asn Lys Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu
 705 710 715 720
 Leu Ala Lys Lys Asn Ala Gly Asp Ala Thr Asp Thr Asp Lys Pro Lys
 725 730 735
 Glu Lys Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu
 740 745 750
 Ala Ser Lys Glu Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu
 755 760 765
 Pro Asp Tyr Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln
 770 775 780
 Leu Ala Gln Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro
 785 790 795 800
 Glu Gly Val Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp
 805 810 815
 Ile Lys Thr Leu Gln Gln Ile Asn Pro
 820 825

<210> 3
 <211> 2379
 <212> DNA
 <213> Streptococcus pyogenes

<400> 3
atgaaaacga aaaaagttat tatttttagt ggtcttattgt tatcatctca gttgactttg 60
atagcttgc aatcacgagg taatggtaca tatccatta aaacgaaaca atcacgtaag 120
ggaatgacgt caaacaaaat taaaccgatt aaaaaaagca aaaagacaaa caagactcac 180
aaagggtgtgg cggggtgtcgta ttttcctaca gatgatgggt ttatTTtaac caaagactca 240
aaaatcttata caaaaacaga tcagggaaatc gttgttgacc atgatggtca ttgcatttt 300
atTTTTatc cggattaaa gggaaagtcca ttGAatacc ttattccaaa aggagcaagt 360
ttAGCTAAGC cagctgtgc tcagcgagca gctagtcaag ggacttctaa agtagcagat 420
cctcatcacc attatgaatt taACCCAGCG gatattgtgg ctGAAGATGC tttAGGCTAC 480
acggttcgcc acgatgatca ctTCCATTAT atTTGAAGT caagcttatac aggtcagaca 540
caggcacaag ctaaacaggt tgctactcgc ttGCCACAAA ccAGTAGCCT tGTTCAACA 600
gctacagcta atGGTATTCC aggcttgcatt ttcccAACCT cagatggTT tcaatttaac 660
ggtcaaggta ttGTTGGGT aacaaaAGAC agtattttAG tggaccacga tGTCACTTA 720
catccattt ctTTTGCgGA cttcgtcag ggtggctgg cacatgtggc agatcaatac 780
gatcccGCTA aaaaAGCAGA aaAGCAGCA gaaACCCATC agacaccaga gctatctgaa 840
cgtgaaaagg aataccaaga aaaattAGCT tatttggcag aaaaatttggg gattgatcca 900
tcaacttata aacgtgtgga aacacaAGAC ggtAAACTTG gtttGAATA ccCTCACCAT 960
gaccacgcac acgtattgtat gttatctgtat attgaaatcg gaaaAGACAT tccAGATCCA 1020
catgttatttgc acgtatGCCG tgaattggaa aacataagg ttGGAATGGA tacTTGCGT 1080
gccttagggT ttGATGAAGA agtGATTtG gatatGTTc GCACTCACGA tGTCACCAACC 1140
caatTTGACT tgggcAGCCG taaAGATCCT ttGCAACGTA aaggacttC actGTTACCC 1200
aacttagaaa ctttaggaat tggcttaca ccaatcaaAG atatctcacc tGTTTGCAA 1260
ttaaaaaaat tgaacAGTT gttaatgaca aaaacAGGGG tgactgatta tagattttG 1320
gataatATGC cacagttaga aggcatTTGAT atttcacaaa acaatCTCAA agatattAGT 1380
ttcttgAGCA aatataaaaaa cttaactcta gtAGCGGCTG ctGATAATGG tattGAAGAT 1440
attaggCCGc ttggTCaatt accaaatCTC aaattCTCG tattGAGTAA caataAGATT 1500
tctgatttaa gcccactGGC atcgTTACAT caattGCAAG aattGcacat tgataataat 1560
cagattacAG attaAGCC tGTTTCTCAT aaAGAAATCAT tgacGGTTG tGATTATCA 1620
agaaatGCTG atGTTGACTT AGCAACACTT caAGCACCA aattAGAAAC gttaatGGTC 1680
aatgatacca aggtttCTCA tttggatttC ttGAAAATA atCCTAATCT atCTAGCTA 1800
tctattaacc gtGCGCAATT GCAATCTCTT gaaggTTG aAGCAAGTAG CGTCATTGTC 1860
agagtGAAG cagaAGGTTA CCAAATTAAA tGCTTGTGC ttaaAGACAA gcaAGGGTC 1920
cttactttct tggatgtgac aggcaaccAG ttGACTTCTC tagaAGGTGT taataatTT 1980
acagcacttG acatTTTAAG cgtGTCTAAA aaccaattaa caaatGTCaa CCTATCTAA 2040
cccaataaga cagttaactaa cattgatatt agtCATAACA atatCTCATT agcAGACCT 2100
aaattGAACG agcaacatAT tccAGAAGCC attGCGAAAA ACTTCCAGC ggtttacGAA 2160
gTTTCTATGG tagGTAATGG aacAGCTGAA gaaaaAGCAG CTATGGCTAC taaggcGAAA 2220
gaaAGTGTc AAGAAGCAtC ggaatcacat gactacaACC AtaAtCAtAC CTATGAAGAT 2280
gaagaAGGTC atGCTCACGA GCAcAGAGAC AAAGATGATC AGGACCATGA ACATGAGGAT 2340
gaaaatGAAG ctaaAGATGA GCAAAACCAT GCTGACTAA 2379

<210> 4

<211> 792

<212> PRT

<213> *Streptococcus pyogenes*

<400> 4
Met Lys Thr Lys Lys Val Ile Ile Leu Val Gly Leu Leu Leu Ser Ser
1 5 10 15
Gln Leu Thr Leu Ile Ala Cys Gln Ser Arg Gly Asn Gly Thr Tyr Pro
20 25 30
Ile Lys Thr Lys Gln Ser Arg Lys Gly Met Thr Ser Asn Lys Ile Lys
35 40 45
Pro Ile Lys Lys Ser Lys Lys Thr Asn Lys Thr His Lys Gly Val Ala
50 55 60
Gly Val Asp Phe Pro Thr Asp Asp Gly Phe Ile Leu Thr Lys Asp Ser
65 70 75 80
Lys Ile Leu Ser Lys Thr Asp Gln Gly Ile Val Val Asp His Asp Gly
85 90 95
His Ser His Phe Ile Phe Tyr Ala Asp Leu Lys Gly Ser Pro Phe Glu
100 105 110
Tyr Leu Ile Pro Lys Gly Ala Ser Leu Ala Lys Pro Ala Val Ala Gln
115 120 125
Arg Ala Ala Ser Gln Gly Thr Ser Lys Val Ala Asp Pro His His His
130 135 140
Tyr Glu Phe Asn Pro Ala Asp Ile Val Ala Glu Asp Ala Leu Gly Tyr
145 150 155 160
Thr Val Arg His Asp Asp His Phe His Tyr Ile Leu Lys Ser Ser Leu
165 170 175
Ser Gly Gln Thr Gln Ala Gln Ala Lys Gln Val Ala Thr Arg Leu Pro
180 185 190
Gln Thr Ser Ser Leu Val Ser Thr Ala Thr Ala Asn Gly Ile Pro Gly
195 200 205
Leu His Phe Pro Thr Ser Asp Gly Phe Gln Phe Asn Gly Gln Gly Ile
210 215 220
Val Gly Val Thr Lys Asp Ser Ile Leu Val Asp His Asp Gly His Leu
225 230 235 240
His Pro Ile Ser Phe Ala Asp Leu Arg Gln Gly Gly Trp Ala His Val
245 250 255

DRAFT

Ala Asp Gln Tyr Asp Pro Ala Lys Lys Ala Glu Lys Pro Ala Glu Thr
260 265 270
His Gln Thr Pro Glu Leu Ser Glu Arg Glu Lys Glu Tyr Gln Glu Lys
275 280 285
Leu Ala Tyr Leu Ala Glu Lys Leu Gly Ile Asp Pro Ser Thr Ile Lys
290 295 300
Arg Val Glu Thr Gln Asp Gly Lys Leu Gly Leu Glu Tyr Pro His His
305 310 315 320
Asp His Ala His Val Leu Met Leu Ser Asp Ile Glu Ile Gly Lys Asp
325 330 335
Ile Pro Asp Pro His Ala Ile Glu His Ala Arg Glu Leu Glu Lys His
340 345 350
Lys Val Gly Met Asp Thr Leu Arg Ala Leu Gly Phe Asp Glu Glu Val
355 360 365
Ile Leu Asp Ile Val Arg Thr His Asp Ala Pro Thr Pro Phe Pro Ser
370 375 380
Asn Glu Lys Asp Pro Asn Met Met Lys Glu Trp Leu Ala Thr Val Ile
385 390 395 400
Lys Leu Asp Leu Gly Ser Arg Lys Asp Pro Leu Gln Arg Lys Gly Leu
405 410 415
Ser Leu Leu Pro Asn Leu Glu Thr Leu Gly Ile Gly Phe Thr Pro Ile
420 425 430
Lys Asp Ile Ser Pro Val Leu Gln Phe Lys Lys Leu Lys Gln Leu Leu
435 440 445
Met Thr Lys Thr Gly Val Thr Asp Tyr Arg Phe Leu Asp Asn Met Pro
450 455 460
Gln Leu Glu Gly Ile Asp Ile Ser Gln Asn Asn Leu Lys Asp Ile Ser
465 470 475 480
Phe Leu Ser Lys Tyr Lys Asn Leu Thr Leu Val Ala Ala Ala Asp Asn
485 490 495
Gly Ile Glu Asp Ile Arg Pro Leu Gly Gln Leu Pro Asn Leu Lys Phe
500 505 510

D E S T R U C T I O N D A T A

Leu Val Leu Ser Asn Asn Lys Ile Ser Asp Leu Ser Pro Leu Ala Ser
515 520 525

Leu His Gln Leu Gln Glu Leu His Ile Asp Asn Asn Gln Ile Thr Asp
530 535 540

Leu Ser Pro Val Ser His Lys Glu Ser Leu Thr Val Val Asp Leu Ser
545 550 555 560

Arg Asn Ala Asp Val Asp Leu Ala Thr Leu Gln Ala Pro Lys Leu Glu
565 570 575

Thr Leu Met Val Asn Asp Thr Lys Val Ser His Leu Asp Phe Leu Lys
580 585 590

Asn Asn Pro Asn Leu Ser Ser Leu Ser Ile Asn Arg Ala Gln Leu Gln
595 600 605

Ser Leu Glu Gly Ile Glu Ala Ser Ser Val Ile Val Arg Val Glu Ala
610 615 620

Glu Gly Asn Gln Ile Lys Ser Leu Val Leu Lys Asp Lys Gln Gly Ser
625 630 635 640

Leu Thr Phe Leu Asp Val Thr Gly Asn Gln Leu Thr Ser Leu Glu Gly
645 650 655

Val Asn Asn Phe Thr Ala Leu Asp Ile Leu Ser Val Ser Lys Asn Gln
660 665 670

Leu Thr Asn Val Asn Leu Ser Lys Pro Asn Lys Thr Val Thr Asn Ile
675 680 685

Asp Ile Ser His Asn Asn Ile Ser Leu Ala Asp Leu Lys Leu Asn Glu
690 695 700

Gln His Ile Pro Glu Ala Ile Ala Lys Asn Phe Pro Ala Val Tyr Glu
705 710 715 720

Gly Ser Met Val Gly Asn Gly Thr Ala Glu Glu Lys Ala Ala Met Ala
725 730 735

Thr Lys Ala Lys Glu Ser Ala Gln Glu Ala Ser Glu Ser His Asp Tyr
740 745 750

Asn His Asn His Thr Tyr Glu Asp Glu Glu Gly His Ala His Glu His
755 760 765

Arg Asp Lys Asp Asp His Asp His Glu His Glu Asp Glu Asn Glu Ala
 770 775 780

Lys Asp Glu Gln Asn His Ala Asp
785 790

<210> 5
<211> 2469
<212> DNA
<213> *Streptococcus agalactiae*

<400> 5
gtgaagaaaa catatggta tatcggtca gttgctgcta ttttactgc tactcatatt 60
ggaagtacc agcttggtaa gcatcatatg ggtctagcaa caaaggacaa tcagattgcc 120
tatattgtat atagcaaagg taaggtaaa gcccctaaaa caaacaaaac gatggatcaa 180
atcagtgtg aagaaggcat ctctgctgaa cagatcgtag tcaaaaattac tgaccaaggt 240
tatgttacct cacacggta ccattatcat tttacaatg ggaaagtcc ttatgtgcg 300
attattagt aagagtgtt gatgacggat cctaattacc attttaaaca atcagacgtt 360
atcaatgaaa tcttagacgg ttacgttatt aaagtcaatg gcaactatta tgttcaccc 420
aagccaggt ataagcgtaa aaacattcga accaaacaac aaattgtcga gcaagtagcc 480
aaaggaacta aagaagctaa agaaaaaaggt ttagctcaag tggcccatct cagtaagaa 540
gaagttgcgg cagtcaatga agcaaaaaaga caaggacgct atactacaga cgatggctat 600
attttagtc cgacagatat cattgtatgt ttaggagatg cttatttagt acctcatgtt 660
aatcaatcattatattcc taaaaaagat ttgtctccaa gtgagctgc tgctgcacaa 720
gcctactgga gtcaaaaaca aggtcgaggt gctagaccgt ctgattaccg cccgacacca 780
gccccaggcgtc gtaggaaagc cccaaattccct gatgtgacgc ctaaccctgg acaaggtcat 840
cagccagata acgggtggta tcatccagcg cctccttaggc caaatgtgc gtcacaaaaac 900
aaacacccaa gagatgagtt taaaggaaaa acctttaagg aacttttaga tcaactacac 960
cgtcttgatt tgaatattcc tcatgtggaa gaagatgggt tgattttga accgactcaa 1020
gtgatcaaat caaacgctt tgggtatgt gtcctcatg gagatcatta tcatattatc 1080
ccaagaagtc agttatcacc acttggaaatg gaatttagc atcgatactt accggccaa 1140
actgatgaca acgactcagg ttcagatcac tcaaaaaccat cagataaaga agtgacacat 1200
accttcttg gtcatcgcat caaagcttac ggaaaaggct tagatggtaa accatatgt 1260
acgagtgtatg cttatgttt tagtaagaa tccattcatt cagtgatgatc accaggagtt 1320
acagctaaac acggagatca tttccactat ataggattt gagaacttga acaatatgt 1380
ttggatgagg tgcgtaactg ggtgaaaagca aaaggtcaag ctgatgagct tggtctgc 1440
ttggatcagg aacaaggcaa agaaaaaccat ctcttgaca ctaaaaaagt gagtcgcaaa 1500
gtaacaaaag atggtaaagt gggctatatt atgccaaaag atggcaagga ctatttctat 1560
gctcggttac aacttgattt gactcagatt gccttgccg aacaagaact aatgcttaaa 1620
gataagaagc attaccgtt tgacattgtt gatacaggca ttgagccacg acttgctgt 1680
gatgtgtcaa gtctgcccgt gcatgttgtt aatgtctactt acgatactgg aagttcgat 1740
gttatcccac atattgtatca tatccatgtc gttccgtatt catggttgac ggcacatcag 1800
attgcaacaa tcaagtatgt gatgcaacac cccgaagtcc gtccggatgtt atggcttaag 1860
ccagggcatg aagagtccagg ttcggtcatt ccaaatgtt cgccttgc taaacgtgt 1920
ggtatgccaa actggcaaat tatcattct gctgaagaag ttcaaaaagc cctagcagaa 1980
qgtcgatccatc cggctatatt ttcgatccac gagatgtttt ggcaaaaagaa 2040

acttttgtat ggaaagatgg ctcccttagc atcccaagag cagatggcag ttcattgaga 2100
accattaata aatccgatct atcccaagct gagtggcaac aagctcaaga gttattggca 2160
aagaaaaatg ctggtgatgc tactgatacg gataaacctg aagaaaaagca acaggcagat 2220
aagagcaatg aaaaccaaca gccaaagtgaa gccagtaaag aagaaaaaga atcagatgac 2280
ttttagaca gtttaccaga ctatggtcta gatagagcaa ccctagaaga tcatatcaat 2340
caatttagcac aaaaagctaa tatcgatct aagtatctca ttttccaacc agaagggtgtc 2400
caattttata ataaaaatgg tgaattggta acttatgata tcaagacact tcaacaaata 2460
2469
aacccttaa

<210> 6
<211> 822
<212> PRT
<213> Streptococcus agalactiae

<400> 6
Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
1 5 10 15
Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Leu
20 25 30
Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
35 40 45
Val Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu
50 55 60
Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
65 70 75 80
Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val
85 90 95
Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
100 105 110
Tyr His Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
115 120 125
Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
130 135 140
Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
145 150 155 160
Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
165 170 175

Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
180 185 190
Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
195 200 205
Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
210 215 220
Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
225 230 235 240
Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
245 250 255
Arg Pro Thr Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro Asp Val
260 265 270
Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly Tyr His
275 280 285
Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His Gln Arg
290 295 300
Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln Leu His
305 310 315 320
Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu Ile Phe
325 330 335
Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val Val Pro
340 345 350
His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser Pro Leu
355 360 365
Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Asp Asn
370 375 380
Asp Ser Gly Ser Asp His Ser Lys Pro Ser Asp Lys Glu Val Thr His
385 390 395 400
Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu Asp Gly
405 410 415
Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu Ser Ile
420 425 430

His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
435 440 445

His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
450 455 460

Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Val Ala Ala
Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Val Ala Ala
465 470 475 480

Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
485 490 495

Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Ile Met Pro
Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Ile Met Pro
500 505 510

Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Tyr Gln Leu Asp Leu Thr
Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Tyr Gln Leu Asp Leu Thr
515 520 525

Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Lys His
Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Lys His
530 535 540

Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
545 550 555 560

Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
565 570 575

Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
580 585 590

Tyr Ser Trp Leu Thr Arg Asn Gln Ile Ala Thr Ile Lys Tyr Val Met
Tyr Ser Trp Leu Thr Arg Asn Gln Ile Ala Thr Ile Lys Tyr Val Met
595 600 605

Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
610 615 620

Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
625 630 635 640

Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Val Gln Lys
Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Val Gln Lys
645 650 655

Ala Leu Ala Glu Gly Arg Phe Ala Ala Pro Asp Gly Tyr Ile Phe Asp
Ala Leu Ala Glu Gly Arg Phe Ala Ala Pro Asp Gly Tyr Ile Phe Asp
660 665 670

Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
675 680 685

Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile Asn Lys
 690 695 700
 Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu Leu Ala
 705 710 715 720
 Lys Lys Asn Ala Gly Asp Ala Thr Asp Thr Asp Lys Pro Glu Glu Lys
 725 730 735
 Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu Ala Ser
 740 745 750
 Lys Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu Pro Asp Tyr
 755 760 765
 Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln Leu Ala Gln
 770 775 780
 Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro Glu Gly Val
 785 790 795 800
 Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp Ile Lys Thr
 805 810 815
 Leu Gln Gln Ile Asn Pro
 820

Digitized by srujanika@gmail.com